



IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Application of:

Green et al.

Serial No. 09/837,751

Filed: April 18, 2001

For: METHOD OF MODIFYING THE  
CONTENT OF COTTONSEED OIL

:

: Group Art Unit: 1651

: Examiner: Not yet assigned

:

#5

STATEMENT UNDER 37 C.F.R. §1.821-824

Commissioner for Patents  
BOX MISSING PARTS  
Washington, D.C. 20231

Sir:

The above-identified patent application contained sequences as defined in 37 C.F.R. §1.821(a). Accordingly, the specification included a paper copy of Sequence Listing as pages 1 - 25. In response to Notice to File Missing Parts of Nonprovisional Application filed herewith, that paper copy (pages 1 - 25) is being cancelled and a substitute paper (pages 1 - 30) is provided herewith. Applicants also submit a write-protected diskette copy of the replacement Sequence Listing in computer-readable form as required by 37 C.F.R. §1.821(e).

In compliance with 37 C.F.R. §1.821(f), the undersigned states that the content of the substitute paper copy and computer-readable copy of the Sequence Listing as enclosed herewith, are the same.

Respectfully submitted,

Donna M. Ferber  
Reg. No. 33,878

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Attorney Docket No.: 45-00  
bmk: November 1, 2001

**CERTIFICATE OF MAILING**

I hereby certify that this correspondence is being deposited with the United States Postal Service with sufficient postage as first class mail in an envelope addressed to the Commissioner for Patents, Washington, D.C., 20231

1 November 2001 B. Kroge  
Date B. Kroge



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# SEQUENCE LISTING

<110> Green, Allan  
Singh, Surinder  
Liu, Qing

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<140> 09/837,751

<141> 2001-04-18

<150> US 60/198,124

<151> 2000-04-18

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<170> PatentIn Ver. 2.0

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Met Gly Ala Gly Gly Arg Met Ser Val Pro Thr Ser Pro Lys Lys Pro  
 1 5 10 15

Glu Phe Asn Ser Leu Lys Arg Val Pro Tyr Ser Lys Pro Pro Phe Thr  
 20 25 30

Leu Ser Glu Ile Lys Lys Ala Ile Pro Pro His Cys Phe Gln Arg Ser  
 35 40 45

Val Leu Arg Ser Phe Ser Tyr Leu Leu Tyr Asp Phe Ile Leu Ala Ser  
 50 55 60

Leu Phe Tyr His Val Ala Thr Asn Tyr Phe Pro Asn Leu Pro Gln Ala  
 65 70 75 80

Leu Ser Asn Val Ala Trp Pro Leu Tyr Trp Ala Met Gln Gly Cys Ile  
 85 90 95

Leu Thr Gly Val Trp Val Ile Ala His Glu Cys Gly His His Ala Phe  
 100 105 110  
 Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Leu His Ser  
 115 120 125  
 Ser Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Arg His  
 130 135 140  
 His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys  
 145 150 155 160  
 Lys Lys Ser Gly Leu Arg Trp Trp Ala Lys His Phe Asn Asn Pro Pro  
 165 170 175  
 Gly Arg Phe Leu Ser Ile Thr Ile Gln Leu Thr Leu Gly Trp Pro Leu  
 180 185 190  
 Tyr Leu Ala Phe Asn Val Ala Gly Arg Pro Tyr Asp Arg Phe Ala Cys  
 195 200 205  
 His Tyr Asp Pro Tyr Gly Pro Ile Phe Ser Asp Arg Glu Arg Leu Gln  
 210 215 220  
 Ile Tyr Ile Ser Asp Ala Gly Val Leu Ala Val Ala Tyr Ala Leu Tyr  
 225 230 235 240  
 Arg Leu Val Leu Ala Lys Gly Val Gly Trp Val Ile Ser Val Tyr Gly  
 245 250 255  
 Val Pro Leu Leu Val Val Asn Ala Phe Leu Val Met Ile Thr Tyr Leu  
 260 265 270  
 Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Ser Glu Trp Asp  
 275 280 285  
 Trp Met Arg Gly Ala Leu Ser Thr Val Asp Arg Asp Tyr Gly Ile Leu  
 290 295 300  
 Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His Leu  
 305 310 315 320  
 Phe Ser Thr Met Pro His Tyr His Ala Met Val Ala Thr Lys Ala Ile  
 325 330 335  
 Lys Pro Ile Leu Gly Glu Tyr Tyr Gln Phe Asp Gly Met Pro Val Tyr  
 340 345 350  
 Lys Ala Ile Trp Arg Glu Ala Lys Glu Cys Leu Tyr Val Glu Pro Asp  
 355 360 365

Glu Gly Asp Lys Asp Lys Gly Val Phe Trp Phe Arg Asn Lys Leu  
 370 375 380

<210> 7  
 <211> 5006  
 <212> DNA  
 <213> Gossypium sp.

<220>  
 <221> 5'UTR  
 <222> (3785)..(5006)

<220>  
 <221> intron  
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<400> 7  
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 aaaggcccaa ctaatccaaa caaaacttga gtgttacaat ctaaccctag tctggcaacg 180  
 gatacggggtt aagggtgtta caacctttac agtgatcaac gaacaaacct tgagtggatt 240  
 tggatttgac cccctaccc cactacacac aaggaagaat gttagtttag ttattcaata 300  
 gctactaagt tggtttacat atatatacaa gttccacact tgattctcaa tcaatgtgag 360  
 actaatgctt ttcattttctc tcaacataat tcacaagtag cttactttga gtatcaattt 420  
 ttcattcatc actcaatcat tttgagcata tgatatattg ttgtaaatgt ctaatggagt 480  
 agaataataa attataat tttatgattcaa cttttcacct ttaccaatag aaaatatgcc 540  
 tcaaagtttt caaaaaatca ttttttttct aatagaaata acttttagaca tcaagaatct 600  
 acgaataaaa tttaaataac tttttttctc aatcttcgat acttgctatt aaattaactt 660  
 aaattcttct acttgagatt ttgatgcatg cgacaaaaat tgagattaga atccatgatg 720  
 tggaaagcaa aacaaatatg taagcaaata ttgtcttgtc gtaaaacat ttgatttttt 780  
 ttttcaatca ttcattgaaa ttgaagtccc tcaatgaagc catcacataa tatgttacat 840  
 aaaagttaga aacttaaacg tgatgatgca tgaacctctc taatttcact ctccaaaatt 900  
 catacagcaa gcgatacttc caatgaccca aaattattga aaccaatgtg cttttcctat 960  
 cattgaaaat cgtgatggag ccacttgtaa cattgtttgc gtacatactt attattatta 1020

ttattattaa tattttattg ataaaagtat tagaaatfff tgtattaaaa gtcagattat 1080  
 attttatatt ttaaaaataa ataagttagt cattctgtgt tagatcaa at agcaaaacaa 1140  
 tagaaataga tgaaatfftc aataaaaaag gaccagttta ctctttgaac taacgcacaa 1200  
 tgactaattt accattttta gtagatgagg taaaatataa tctagctcct tgtacagggg 1260  
 ctccogtgat acttttacc ctttctatct cttctcaacg ataaataaaa atatgtttta 1320  
 gaaaatfftg ttccaaaga taattacaaa gttaagtcaa acaagcagta acattgtttc 1380  
 acttaatffc cctttcgaaa gaaaaactct tatttagaat aattgtcatt caaagtaact 1440  
 atttttttta gaacagctat gcttggaca atcatgttta gaacatggct ccattttaga 1500  
 atatggttgt cgtttgagaa caactcctgc aaaggataac gaatgtttgg aacagtctct 1560  
 atttagaata actgcgtffc aagaataatc atatttagaa caacctccat ttaaaacaat 1620  
 agtggttttt tttaaaaaga agagatatta ttcaaaatta gctctttcaa gaaaagcatc 1680  
 accatagaac aactattatt aaaaataaag ctaaattcac aatttggccc ttgaagtata 1740  
 ctcatftttt gactttggta tctaaacttt tctttgcctc aatttgatac ctaaaatact 1800  
 ctcaaattcc atfttttgac agacattaaa aaaataatct tatagccaat cacaagcgc 1860  
 cacgtggcgt ctttatgtaa aaagaaatat tttgtttaat taaatgtata tacacattaa 1920  
 aaaaataaaa aatatagaac aacatataaa ttataaacia atctataaaa ataaaattta 1980  
 caaaaatata ataattgaaa aaaaattagt tgaaattaat aatattatta aaaaatgtaa 2040  
 aacatttgta aaaattataa aaaagtttta aaaataatft tctttataaa attctaaaat 2100  
 atataattct aaaattgtaa aaaggatat aaatttcatt tttttcaatt actcgaaatt 2160  
 taaatacttt ttcaatfttt ataacacttt tttaatfttt atatattatt ttggattfttt 2220  
 aaaatttata attatatatt tcaaaatftt ataaatfttt ttatatgtta tatatgattt 2280  
 tttacatttt taatcaatat aatataaaat actaaatftt tttaaaaaaa tgatacgtgg 2340  
 catgtttctaa tatcgccaca tgaccggtga acgtcgggtc aatggccagt caaagccaaa 2400  
 agtattfttt taatatttaa ataattaatt ttatacttct atfttttaatt ttaattta at 2460  
 atftttattt taaataaact taattgttat gtgatatttt ttcaactgacc caaaacatgc 2520  
 tatgtggagc ttttccatt agccaaagtt gccaaataga ttttttcaac gtgtgtttaca 2580

aaatggaccg aaaatagagg aaattgatac tttaggtatc aagttgggat aaaaaaagtt 2640  
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 gacaattata ttgagaataa attaggttta gaacgggtca aaataattct tattcagtaa 2760  
 caacttttgt tcaagaacaa ctcttcaata acaaaagttt gtatttcacg agatgctctt 2820  
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 aaatgtcttg attgtgattg taatcttttc ttagttgtac aaatatattg attataattg 2940  
 tgatggaaaa aaataaaaaa aattaaattt tagatgaata aagagtacat gggctataat 3000  
 tagaattaac ctaaatttgt ttggttataa ctagaggttt tggttcaaag aattaatttc 3060  
 taaatccgag tccaaccgc tttggatcag ccaaaggttc ttttaaatta ttttaattat 3120  
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 cgagttaatc caaaattgaa gaatataaac tcaaactcga ctcaagatga atcgaaccgc 3240  
 ttgactaaac tgaccaacc caacttgttt ttgagctaag tttgagttta atattttcaa 3300  
 cttcacgttg gcttgacca gactgattaa ttattaaaca actaaaagaa ttttaataata 3360  
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 gtgattatat gatttatgtt taatttaaat gttaattatt tatatttact tcaacaatag 3480  
 tagtaacatt ctgtaatatg aatatgaatc cgatgattga gaagtgagag gtgttacata 3540  
 tttactaccg aggaatacct ttccttcac gatgaagtcc ttatcgttgc aacagggtgtt 3600  
 tgggagatat caaaaagagg cggggtaatg atgatgatga aagcgagaat catcagaatc 3660  
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 aaaaccactt gattaagctc cccctccgct ccataccact cgcccaaac caacacgcct 3840  
 tctttgcctc gtgtttcacc acctggcggt aaactgcttt ctttaaagggt acatttctct 3900  
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 tttgagtga tgatgtttgg tatatcttct tagtaactga ctttttgaaa atactagcat 4020  
 tttttttaat atcaagtga agaagaagaa gaatttcgcc atgcaaaagc tttttaaggc 4080  
 tttttctttt ccttagatca aaatttatct gtttacttat actgttcttt taagcccgaa 4140

gaaagaagcc atgggtttcaa tttttgagag ttttaaattcc caaataccag agagcttcat 4200  
 cgtttattca tatatatttta aacatttttt aaagcaagaa cttgtgattt gtttttaata 4260  
 aaatatgcaa taaatttttta tatttttctgt aaatttaaaa ttttaatttt ctacttttaa 4320  
 aatttaaaaa agtaaatttt aaaatatacc tttcattaaa tttaaattatt ataagtaatt 4380  
 gagtattttt aatttttaaaa tttcacacat caaatttaaaa aaaaagttaa cacttgccact 4440  
 tgattttgaa aagtaaaagg attaaatttc aaattttcag taaaaggact aaatttcaaa 4500  
 tttttaaaga gtatagagac tctctacat tttagatttt aaaatttaaa tctaacagtt 4560  
 aacactttct taattacttt acgataaatt taactaaaaa attacaatat taatgggttaa 4620  
 aattaaattt tgaaaagtat aaagattaaa ttgtaaattt tcaaaaagca taggaagtta 4680  
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 gtcacctttt gccagtattt tccagtggct tgtttctctc aaaactacct tgaatcttga 4800  
 gacagaatta aatatatttt tggccttttc ttcattttct ctctctctat tttcttttaa 4860  
 aaattgcttt agagaattca gaaaaaatac tttccaacac gaaaatttct tcaaatttat 4920  
 tgtttatata taataaatgg ttgcttaatt ttggaaaaca aaagttattg tagttagttt 4980  
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<210> 8

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthetic  
oligonucleotide useful as a primer

<400> 8

atggcktsa rgctbcatsc

20

<210> 9

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthetic

oligonucleotide useful as a primer

<400> 9  
tcasagyttn acytgyctat 20

<210> 10  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:synthetic  
oligonucleotide useful as a primer

<400> 10  
gcataggtca tggaccacgt 20

<210> 11  
<211> 17  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:synthetic  
oligonucleotide useful as a primer

<400> 11  
gtaaaacgac ggccagt 17

<210> 12  
<211> 19  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:synthetic  
oligonucleotide useful as a primer

<400> 12  
ggaaacagct atgaccatg 19

<210> 13  
<211> 8  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthetic  
oligonucleotide useful as a primer

<400> 13  
ggcccggg

8

<210> 14  
<211> 8  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:synthetic  
oligonucleotide useful as a primer

<400> 14  
ggcccccg

8

<210> 15  
<211> 19  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:synthetic  
oligonucleotide useful as a primer

<400> 15  
ttttaatgcc atgcctcg

19

<210> 16  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:synthetic  
oligonucleotide useful as a primer

<400> 16  
cttcagcagt ccaagccctg

20

<210> 17  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:synthetic  
 oligonucleotide useful as a primer

<400> 17  
 cctggcggtta aactgctttc 20

<210> 18  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:synthetic  
 oligonucleotide useful as a primer

<400> 18  
 ccatatagtt tattaatata acac 24

<210> 19  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:synthetic  
 oligonucleotide useful as a primer

<400> 19  
 tatgttgcaa gtaggtgatc 20

<210> 20  
 <211> 32  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:synthetic  
 oligonucleotide useful as a primer

<400> 20  
 acgcgtcgac gtgtgttaca aaatggaccg aa 32

<210> 21  
 <211> 32  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:synthetic  
 oligonucleotide useful as a primer

<400> 21  
 cgcggatccg ctggctggac acgcaagaag ca 32

<210> 22  
 <211> 27  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:synthetic  
 oligonucleotide useful as a primer

<400> 22  
 cgagctcccc ctccgctcca taccact 27

<210> 23  
 <211> 31  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:synthetic  
 oligonucleotide useful as a primer

<400> 23  
 cgcggatccg ctggctttaa agaaagcagt t 31

<210> 24  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:synthetic  
 oligonucleotide useful as a primer

<400> 24  
 catgtgacag atcgaaggaa 20

<210> 25  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:synthetic  
           oligonucleotide useful as a primer  
  
 <400> 25  
 atctaattat tctattcaga c 21  
  
 <210> 26  
 <211> 6  
 <212> PRT  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence:synthetic  
           peptide  
  
 <220>  
 <221> UNSURE  
 <222> (1)..(6)  
 <223> Xaa at position 3 is either Trp or Cys  
  
 <400> 26  
 His Glu Xaa Gly His His  
   1                  5  
  
 <210> 27  
 <211> 5  
 <212> PRT  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence:synthetic  
           peptide  
  
 <400> 27  
 His Arg Arg His His  
   1                  5  
  
 <210> 28  
 <211> 5  
 <212> PRT  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence:synthetic  
           peptide  
  
 <400> 28

His Val Ala His His  
1 5

<210> 29  
<211> 5  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:synthetic  
peptide

<220>  
<221> UNSURE  
<222> (1)..(5)  
<223> Xaa at position 2 is any amino acid; Xaa at  
position 3 is any amino acid

<400> 29  
His Xaa Xaa His His  
1 5

<210> 30  
<211> 6  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:synthetic  
peptide

<220>  
<221> UNSURE  
<222> (1)..(6)  
<223> Xaa at position 2 is any amino acid; Xaa at  
position 3 is any amino acid; Xaa at position 4 is  
any amino acid

<400> 30  
His Xaa Xaa Xaa His His  
1 5

<210> 31  
<211> 383  
<212> PRT  
<213> Glycine max

<400> 31

Met Gly Ala Gly Gly Arg Thr Asp Val Pro Pro Ala Asn Arg Lys Ser  
1 5 10 15  
Glu Val Asp Pro Leu Lys Arg Val Pro Phe Glu Lys Pro Gln Phe Ser  
20 25 30  
Leu Ser Gln Ile Lys Lys Ala Ile Pro Pro His Cys Phe Gln Arg Ser  
35 40 45  
Val Leu Arg Ser Phe Ser Tyr Val Val Tyr Asp Leu Thr Ile Ala Phe  
50 55 60  
Cys Leu Tyr Tyr Val Ala Thr His Tyr Phe His Leu Leu Pro Gly Pro  
65 70 75 80  
Leu Ser Phe Arg Gly Met Ala Ile Tyr Trp Ala Val Gln Gly Cys Ile  
85 90 95  
Leu Thr Gly Val Trp Val Ile Ala His Glu Cys Gly His His Ala Phe  
100 105 110  
Ser Asp Tyr Gln Leu Leu Asp Asp Ile Val Gly Leu Ile Leu His Ser  
115 120 125  
Ala Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Arg His  
130 135 140  
His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys  
145 150 155 160  
Gln Lys Ser Cys Ile Lys Trp Tyr Ser Lys Tyr Leu Asn Asn Pro Pro  
165 170 175  
Gly Arg Val Leu Thr Leu Ala Val Thr Leu Thr Leu Gly Trp Pro Leu  
180 185 190  
Tyr Leu Ala Leu Asn Val Ser Gly Arg Pro Tyr Asp Arg Phe Ala Cys  
195 200 205  
His Tyr Asp Pro Tyr Gly Pro Ile Tyr Ser Asp Arg Glu Arg Leu Gln  
210 215 220  
Ile Tyr Ile Ser Asp Ala Gly Val Leu Ala Val Val Tyr Gly Leu Phe  
225 230 235 240  
Arg Leu Ala Met Ala Lys Gly Leu Ala Trp Val Val Cys Val Tyr Gly  
245 250 255  
Val Pro Leu Leu Val Val Asn Gly Phe Leu Val Leu Ile Thr Phe Leu  
260 265 270

Gln His Thr His Pro Ala Leu Pro His Tyr Thr Ser Ser Glu Trp Asp  
 275 280 285  
 Trp Leu Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile Leu  
 290 295 300  
 Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His Leu  
 305 310 315 320  
 Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala Thr Lys Ala Ile  
 325 330 335  
 Lys Pro Ile Leu Gly Glu Tyr Tyr Arg Phe Asp Glu Thr Pro Phe Val  
 340 345 350  
 Lys Ala Met Trp Arg Glu Ala Arg Glu Cys Ile Tyr Val Glu Pro Asp  
 355 360 365  
 Gln Ser Thr Glu Ser Lys Gly Val Phe Trp Tyr Asn Asn Lys Leu  
 370 375 380

<210> 32  
 <211> 383  
 <212> PRT  
 <213> Arabidopsis thaliana

<400> 32  
 Met Gly Ala Gly Gly Arg Met Pro Val Pro Thr Ser Ser Lys Lys Ser  
 1 5 10 15  
 Glu Thr Asp Thr Thr Lys Arg Val Pro Cys Glu Lys Pro Pro Phe Ser  
 20 25 30  
 Val Gly Asp Leu Lys Lys Ala Ile Pro Pro His Cys Phe Lys Arg Ser  
 35 40 45  
 Ile Pro Arg Ser Phe Ser Tyr Leu Ile Ser Asp Ile Ile Ile Ala Ser  
 50 55 60  
 Cys Phe Tyr Tyr Val Ala Thr Asn Tyr Phe Ser Leu Leu Pro Gln Pro  
 65 70 75 80  
 Leu Ser Tyr Leu Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Cys Val  
 85 90 95  
 Leu Thr Gly Ile Trp Val Ile Ala His Glu Cys Gly His His Ala Phe  
 100 105 110  
 Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser  
 115 120 125

Phe	Leu	Leu	Val	Pro	Tyr	Phe	Ser	Trp	Lys	Tyr	Ser	His	Arg	Arg	His	130	135	140	
His	Ser	Asn	Thr	Gly	Ser	Leu	Glu	Arg	Asp	Glu	Val	Phe	Val	Pro	Lys	145	150	155	160
Gln	Lys	Ser	Ala	Ile	Lys	Trp	Tyr	Gly	Lys	Tyr	Leu	Asn	Asn	Pro	Leu	165	170	175	
Gly	Arg	Ile	Met	Met	Leu	Thr	Val	Gln	Phe	Val	Leu	Gly	Trp	Pro	Leu	180	185	190	
Tyr	Leu	Ala	Phe	Asn	Val	Ser	Gly	Arg	Pro	Tyr	Asp	Gly	Phe	Ala	Cys	195	200	205	
His	Phe	Phe	Pro	Asn	Ala	Pro	Ile	Tyr	Asn	Asp	Arg	Glu	Arg	Leu	Gln	210	215	220	
Ile	Tyr	Leu	Ser	Asp	Ala	Gly	Ile	Leu	Ala	Val	Cys	Phe	Gly	Leu	Tyr	225	230	235	240
Arg	Tyr	Ala	Ala	Ala	Gln	Gly	Met	Ala	Ser	Met	Ile	Cys	Leu	Tyr	Gly	245	250	255	
Val	Pro	Leu	Leu	Ile	Val	Asn	Ala	Phe	Leu	Val	Leu	Ile	Thr	Tyr	Leu	260	265	270	
Gln	His	Thr	His	Pro	Ser	Leu	Pro	His	Tyr	Asp	Ser	Ser	Glu	Trp	Asp	275	280	285	
Trp	Leu	Arg	Gly	Ala	Leu	Ala	Thr	Val	Asp	Arg	Asp	Tyr	Gly	Ile	Leu	290	295	300	
Asn	Lys	Val	Phe	His	Asn	Ile	Thr	Asp	Thr	His	Val	Ala	His	His	Leu	305	310	315	320
Phe	Ser	Thr	Met	Pro	His	Tyr	Asn	Ala	Met	Glu	Ala	Thr	Lys	Ala	Ile	325	330	335	
Lys	Pro	Ile	Leu	Gly	Asp	Tyr	Tyr	Gln	Phe	Asp	Gly	Thr	Pro	Trp	Tyr	340	345	350	
Val	Ala	Met	Tyr	Arg	Glu	Ala	Lys	Glu	Cys	Ile	Tyr	Val	Glu	Pro	Asp	355	360	365	
Arg	Glu	Gly	Asp	Lys	Lys	Gly	Val	Tyr	Trp	Tyr	Asn	Asn	Lys	Leu	370	375	380		

<210> 33  
<211> 387

<212> PRT

<213> Glycine max

<400> 33

Met Gly Leu Ala Lys Glu Thr Thr Met Gly Gly Arg Gly Arg Val Ala  
1 5 10 15

Lys Val Glu Val Gln Gly Lys Lys Pro Leu Ser Arg Val Pro Asn Thr  
20 25 30

Lys Pro Pro Phe Thr Val Gly Gln Leu Lys Lys Ala Ile Pro Pro His  
35 40 45

Cys Phe Gln Arg Ser Leu Leu Thr Ser Phe Ser Tyr Val Val Tyr Asp  
50 55 60

Leu Ser Phe Ala Phe Ile Phe Tyr Ile Ala Thr Thr Tyr Phe His Leu  
65 70 75 80

Leu Pro Gln Pro Phe Ser Leu Ile Ala Trp Pro Ile Tyr Trp Val Leu  
85 90 95

Gln Gly Cys Leu Leu Thr Gly Val Trp Val Ile Ala His Glu Cys Gly  
100 105 110

His His Ala Phe Ser Lys Tyr Gln Trp Val Asp Asp Val Val Gly Leu  
115 120 125

Thr Leu His Ser Thr Leu Leu Val Pro Tyr Phe Ser Trp Lys Ile Ser  
130 135 140

His Arg Arg His His Ser Asn Thr Gly Ser Leu Asp Arg Asp Glu Val  
145 150 155 160

Phe Val Pro Lys Pro Lys Ser Lys Val Ala Trp Phe Ser Lys Tyr Leu  
165 170 175

Asn Asn Pro Leu Gly Arg Ala Val Ser Leu Leu Val Thr Leu Thr Ile  
180 185 190

Gly Trp Pro Met Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp  
195 200 205

Ser Phe Ala Ser His Tyr His Pro Tyr Ala Pro Ile Tyr Ser Asn Arg  
210 215 220

Glu Arg Leu Leu Ile Tyr Val Ser Asp Val Ala Leu Phe Ser Val Thr  
225 230 235 240

Tyr Ser Leu Tyr Arg Val Ala Thr Leu Lys Gly Leu Val Trp Leu Leu  
245 250 255

Cys Val Tyr Gly Val Pro Leu Leu Ile Val Asn Gly Phe Leu Val Thr  
 260 265 270  
 Ile Thr Tyr Leu Gln His Thr His Phe Ala Leu Pro His Tyr Asp Ser  
 275 280 285  
 Ser Glu Trp Asp Trp Leu Lys Gly Ala Leu Ala Thr Met Asp Arg Asp  
 290 295 300  
 Tyr Gly Ile Leu Asn Lys Val Phe His His Ile Thr Asp Thr His Val  
 305 310 315 320  
 Ala His His Leu Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala  
 325 330 335  
 Thr Asn Ala Ile Lys Pro Ile Leu Gly Glu Tyr Tyr Gln Phe Asp Asp  
 340 345 350  
 Thr Pro Phe Tyr Lys Ala Leu Trp Arg Glu Ala Arg Glu Cys Leu Tyr  
 355 360 365  
 Val Glu Pro Asp Glu Gly Thr Ser Glu Lys Gly Val Tyr Trp Tyr Arg  
 370 375 380  
 Asn Lys Tyr  
 385

<210> 34  
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 <212> PRT  
 <213> Brassica napus

<400> 34  
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 Phe Asp Pro Ser Ala Gln Pro Pro Phe Lys Ile Gly Asp Ile Arg Ala  
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 Ala Ile Pro Lys His Cys Trp Val Lys Ser Pro Leu Arg Ser Met Ser  
 35 40 45  
 Tyr Val Ala Arg Asp Ile Phe Ala Val Val Ala Leu Ala Val Ala Ala  
 50 55 60  
 Val Tyr Phe Asp Ser Trp Phe Phe Trp Pro Leu Tyr Trp Ala Ala Gln  
 65 70 75 80  
 Gly Thr Leu Phe Trp Ala Ile Phe Val Leu Gly His Asp Cys Gly His  
 85 90 95

Gly Ser Phe Ser Asp Ile Pro Leu Leu Asn Thr Ala Val Gly His Ile  
 100 105 110  
 Leu His Ser Phe Ile Leu Val Pro Tyr His Gly Trp Arg Ile Ser His  
 115 120 125  
 Arg Thr His His Gln Asn His Gly His Val Glu Asn Asp Glu Ser Trp  
 130 135 140  
 Val Pro Leu Pro Glu Lys Leu Tyr Lys Asn Leu Ser His Ser Thr Arg  
 145 150 155 160  
 Met Leu Arg Tyr Thr Val Pro Leu Pro Met Leu Ala Tyr Pro Leu Tyr  
 165 170 175  
 Leu Trp Tyr Arg Ser Pro Gly Lys Glu Gly Ser His Tyr Asn Pro Tyr  
 180 185 190  
 Ser Ser Leu Phe Ala Pro Ser Glu Arg Lys Leu Ile Ala Thr Ser Thr  
 195 200 205  
 Thr Cys Trp Ser Ile Met Leu Ala Thr Leu Val Tyr Leu Ser Phe Leu  
 210 215 220  
 Val Gly Pro Val Thr Val Leu Lys Val Tyr Gly Val Pro Tyr Ile Ile  
 225 230 235 240  
 Phe Val Met Trp Leu Asp Ala Val Thr Tyr Leu His His His Gly His  
 245 250 255  
 Asp Asp Lys Leu Pro Trp Tyr Arg Gly Lys Glu Trp Ser Tyr Leu Arg  
 260 265 270  
 Gly Gly Leu Thr Thr Ile Asp Arg Asp Tyr Gly Ile Phe Asn Asn Ile  
 275 280 285  
 His His Asp Ile Gly Thr His Val Ile His His Leu Phe Pro Gln Ile  
 290 295 300  
 Pro His Tyr His Leu Val Asp Ala Thr Lys Ser Ala Lys His Val Leu  
 305 310 315 320  
 Gly Arg Tyr Tyr Arg Glu Pro Lys Thr Ser Gly Ala Ile Pro Ile His  
 325 330 335  
 Leu Val Glu Ser Leu Val Ala Ser Ile Lys Lys Asp His Tyr Val Ser  
 340 345 350  
 Asp Thr Gly Asp Ile Val Phe Tyr Glu Thr Asp Pro Asp Leu Tyr Val  
 355 360 365

Tyr Ala Ser Asp Lys Ser Lys Ile Asn  
 370 375

<210> 35  
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<400> 35  
 Met Ala Cys Thr Leu Ala Asp Ser Leu Leu Leu Phe Lys Gly Ser Tyr  
 1 5 10 15

Gln Lys Pro Val Leu Arg Arg Asp Ile Ala Ala Arg Tyr Ser Pro Gly  
 20 25 30

Ile Phe Ser Leu Asn Ser Asn Gly Leu Ile Gln Lys Arg Phe Arg Arg  
 35 40 45

Gln Arg Asn Phe Val Thr Arg Asn Lys Val Thr Val Ile His Ala Val  
 50 55 60

Ala Ile Pro Val Gln Pro Ala Pro Val Glu Ser Ala Glu Tyr Arg Lys  
 65 70 75 80

Gln Leu Ala Glu Asp Tyr Gly Phe Arg Gln Val Gly Glu Pro Leu Ser  
 85 90 95

Asp Asp Val Thr Leu Lys Asp Val Ile Asn Pro Leu Pro Lys Glu Val  
 100 105 110

Phe Glu Ile Asp Asp Val Lys Ala Trp Lys Ser Val Leu Ile Ser Val  
 115 120 125

Thr Ser Tyr Ala Leu Gly Leu Phe Met Ile Ser Lys Ala Pro Trp Tyr  
 130 135 140

Leu Leu Pro Leu Ala Trp Val Trp Thr Gly Thr Ala Ile Thr Gly Phe  
 145 150 155 160

Phe Val Ile Gly His Asp Cys Ala His Arg Ser Phe Ser Ser Asn Lys  
 165 170 175

Leu Val Glu Asp Ile Val Gly Thr Leu Ala Phe Met Pro Leu Ile Tyr  
 180 185 190

Pro Tyr Glu Pro Trp Arg Phe Lys His Asp Arg His His Ala Lys Thr  
 195 200 205

Asn Met Leu Arg Glu Asp Thr Ala Trp His Pro Val Trp Lys Asp Glu  
 210 215 220

Phe	Glu	Ser	Thr	Pro	Leu	Leu	Arg	Lys	Ala	Ile	Ile	Tyr	Gly	Tyr	Gly	225	230	235	240
Pro	Phe	Arg	Cys	Trp	Met	Ser	Ile	Ala	His	Trp	Leu	Met	Trp	His	Phe	245	250	255	
Asp	Leu	Lys	Lys	Phe	Arg	Pro	Ser	Glu	Val	Pro	Arg	Val	Lys	Ile	Ser	260	265	270	
Leu	Ala	Cys	Val	Phe	Ala	Phe	Ile	Ala	Ile	Gly	Trp	Pro	Leu	Ile	Ile	275	280	285	
Tyr	Lys	Thr	Gly	Ile	Met	Gly	Trp	Ile	Lys	Phe	Trp	Leu	Met	Pro	Trp	290	295	300	
Leu	Gly	Tyr	His	Phe	Trp	Met	Ser	Thr	Phe	Thr	Met	Val	His	His	Thr	305	310	315	320
Ala	Pro	Tyr	Ile	Pro	Phe	Lys	Tyr	Ser	Glu	Glu	Trp	Asn	Arg	Ala	Gln	325	330	335	
Ala	Gln	Leu	Asn	Gly	Thr	Val	His	Cys	Asp	Tyr	Pro	Lys	Trp	Ile	Glu	340	345	350	
Ile	Leu	Cys	His	Asp	Ile	Asn	Val	His	Ile	Pro	His	His	Ile	Ser	Pro	355	360	365	
Arg	Ile	Pro	Ser	Tyr	Asn	Leu	Arg	Ala	Ala	His	Lys	Ser	Leu	Gln	Glu	370	375	380	
Asn	Trp	Gly	Gln	Tyr	Leu	Asn	Glu	Ala	Ser	Trp	Asn	Trp	Arg	Leu	Met	385	390	395	400
Lys	Thr	Ile	Met	Thr	Val	Cys	Gln	Val	Tyr	Asp	Lys	Glu	Lys	Ser	Leu	405	410	415	
Cys	Cys	Leu	Arg	Arg	Thr	Cys	Pro	420											